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ACCESS DB # 172942  
PLEASE PRINT CLEARLY

Scientific and Technical Information Center

## SEARCH REQUEST FORM

Requester's Full Name: DAVID GUZO Examiner #: 70677 Date: 11/30/05  
Art Unit: 1636 Phone Number: 2-0767 Serial Number: 10/696282  
Location (Bldg/Room#): Room 2A59 (Mailbox #): 2C70 Results Format Preferred (circle): PAPER DISK  
\*\*\*\*\*

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Date: \_\_\_\_\_

### Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please run a regular + interference sequence  
search on SEQ ID NO: 1 and on a nucleic  
acid sequence which ~~encodes~~ SEQ ID NO: 13.

1- 4718 NA  
2913 - 736 AA

RECEIVED  
NOV 30 2005  
CH/CHEN, LIAISON  
(STIC)

Thanks

2na-05p 12/12/05  
BHL

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OM protein - nucleic search using frame-dependent model

Run on: December 12, 2005, 07:07:34 ; Search time 8012 Seconds  
(without alignments)  
5079.206 Million cell updates/sec

Title: US-10-696-282-13  
Perfect score: 3989

Sequence: 1 MAADGYLPDWLEDNLSGIR.....NGLYTEPRPIGRYLTRPL 736

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 158293336

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pcp -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPMT=pcp -NORM=ext -HARSIZE=500 -MINLEN=0  
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3989	100.0	2211	54	US-10-696-282-12
2	3989	100.0	2211	54	US-10-696-282-12
3	3989	100.0	2211	54	US-10-696-282-12
4	3989	100.0	4718	1	PCT-US02-33629-6
5	3989	100.0	4718	1	PCT-US02-38423-20
6	3989	100.0	4718	1	PCT-US03-11191-3
7	3989	100.0	4718	43	US-10-291-583-6
8	3989	100.0	4718	51	US-10-427-129-1

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# OM protein - nucleic search.

Run on: December 12, 2005, 11:30:19 ; Search time 239 Seconds

(without alignments)  
1151.285 Million cell updates/sec

Title: US-10-696-282-13

Sequence: 1 MADDGYLPMDLENDLSBGR.....NGLYTPRPDTRRYLTRPL 736

## Scoring table:

BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Delop 6.0, Delext 7.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-O=/cg2n\_1/USPTO.spool.p/US10696282/runat 06122005 133344 8538/app query.fasta\_1.90  
-DB=Published Applications NA.New -QWMT=fastap -SUFR=p2n.rnpbn -MINMATCH=0.1  
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-TRAN=human0.cdi -LIST=45 -OCCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0  
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5: /cg2n\_6/prodata/1/pubpna/US10 NEW PUB.seq:\*  
6: /cg2n\_6/prodata/1/pubpna/US11 NEW PUB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3396.5	85.1	4679	7	US-11-184-380-25	Sequence 25, Appl
2	2486.5	62.3	2208	6	US-10-719-311-5	Sequence 5, Appl
3	2481.5	62.2	4768	6	US-10-719-311-1	Sequence 1, Appl
4	2220	55.7	2307	7	US-11-184-380-7	Sequence 7, Appl
5	2220	55.7	4652	7	US-11-184-380-1	Sequence 1, Appl
6	2214	55.5	2264	7	US-11-184-380-8	Sequence 8, Appl
7	2214	55.5	2264	7	US-11-184-380-9	Sequence 9, Appl
8	1830.5	45.9	1800	6	US-10-719-311-17	Sequence 17, Appl

9	1690.5	42.4	1617	6	US-10-719-311-19	Sequence 19, Appl
10	136	3.4	3289	6	US-10-933-025-14	Sequence 14, Appl
11	136	3.4	4286	6	US-10-933-025-13	Sequence 13, Appl
12	132	3.3	3906	6	US-10-131-826A-19	Sequence 19, Appl
13	127.5	3.2	2616	6	US-10-933-025-5	Sequence 5, Appl
14	127.5	3.2	3263	6	US-10-933-025-4	Sequence 4, Appl
15	119	3.0	191684	7	US-11-121-086-2	Sequence 2, Appl
16	118.5	3.0	5296	6	US-10-510-386-217	Sequence 217, App
17	115.5	2.9	3461	6	US-10-131-826A-199	Sequence 199, App
18	112.5	2.8	6245	6	US-10-401-386B-61	Sequence 61, Appl
19	111	2.8	2901	6	US-10-485-517-54	Sequence 38, Appl
20	111	2.8	169495	6	US-11-121-086-61	Sequence 54, Appl
21	111	2.8	153376	7	US-11-121-086-5	Sequence 51, Appl
22	108	2.7	172543	7	US-11-121-086-6	Sequence 6, Appl
23	108	2.7	1068	7	US-11-135-855-21	Sequence 21, Appl
24	107.5	2.7	5665	6	US-10-851-667A-24	Sequence 24, Appl
25	107.5	2.7	4749	6	US-10-821-234-244	Sequence 24, App
26	107	2.7	4770	7	US-11-000-463-7	Sequence 7, Appl
27	107	2.7	5921	7	US-11-186-284-29	Sequence 29, Appl
28	107	2.7	6728	7	US-11-186-284-27	Sequence 27, Appl
29	106	2.7	4965	6	US-10-485-517-43	Sequence 43, Appl
30	106	2.7	6763	7	US-11-080-991-55	Sequence 55, Appl
31	106	2.7	1155	6	US-10-833-270-1	Sequence 1, Appl
32	105.5	2.6	18156	7	US-11-121-086-3	Sequence 3, Appl
33	105.5	2.6	168516	7	US-11-121-086-3	Sequence 1, Appl
34	104.5	2.6	55763	6	US-11-102-240-99	Sequence 99, Appl
35	104	2.6	2436	7	US-10-972-766-1	Sequence 1, Appl
36	103.5	2.6	2197	7	US-11-000-463-225	Sequence 225, App
37	103.5	2.6	169485	7	US-11-121-086-61	Sequence 61, Appl
38	103	2.6	5891	6	US-10-750-185-56614	Sequence 56614, A
39	102.5	2.6	2745	6	US-10-647-956A-5	Sequence 5, Appl
40	102.5	2.6	9454	7	US-11-109-056-1	Sequence 1, Appl
41	102	2.6	2349	6	US-10-972-053-7	Sequence 7, Appl
42	102	2.6	2557	6	US-10-972-053-1	Sequence 1, Appl
43	101.5	2.5	2133	7	US-11-045-802-10	Sequence 10, Appl
44	101.5	2.5	3469	6	US-10-933-025-7	Sequence 7, Appl
45	101.5	2.5	7989	6	US-10-509-921-8	Sequence 8, Appl

## ALIGNMENTS

RESULT 1  
US-11-184-380-25  
; Sequence 25, Application US/11184380  
; Publication No. US2005025089A1  
; GENERAL INFORMATION:  
; APPLICANT: Kocin, Robert M.  
; TITLE OF INVENTION: AAVS NUCLEIC ACIDS  
; FILE REFERENCE: 14014.0323U3  
; CURRENT APPLICATION NUMBER: US/11/184,380  
; CURRENT FILING DATE: 2005-07-19  
; PRIOR APPLICATION NUMBER: PCT/US99/11958  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,029  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 4679  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence; Note =  
US-11-184-380-25

Alignment Scores:  
Pred. No.: 3,156-280  
Score: 3396.50  
Percent Similarity: 90.08%  
Best Local Similarity: 85.15%  
Query Match: 85.15%  
Length: 4679  
Matches: 612  
Conservative: 51  
Mismatch: 72  
Indels: 1

GenCore version 5.1.6  
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OM protein - nucleic search, ~~using the standard model~~

Run on: December 12, 2005, 09:47:27 ; Search time 1262 Seconds

(without alignments)  
4822.712 Million cell updates/sec

Title: US-10-696-282-13  
Perfect score: 3989  
Sequence: 1 MAAAGYLPWLEDNLSGIR.....NGLYTPRPPIGRYLRPL 736

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9793542 segs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
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Database : Published Applications NA Main:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	3989	100.0	4718	US-10-696-261-1	Sequence 1, Appl
6	3989	100.0	4718	US-10-696-282-1	Sequence 1, Appl
7	3989	100.0	4718	US-10-696-900-1	Sequence 1, Appl

8	3989	100.0	4718	US-10-427-129-1	Sequence 1, Appl
9	3989	100.0	4718	US-10-959-017-3	Sequence 3, Appl
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11	3984	99.9	7447	US-10-216-870-11	Sequence 11, Appl
12	3984	99.9	7447	US-10-415-834-11	Sequence 11, Appl
13	3963	99.3	4683	US-10-427-129-6	Sequence 6, Appl
14	3963	99.3	4683	US-10-959-017-2	Sequence 2, Appl
15	3945	98.9	4683	US-10-696-261-19	Sequence 19, Appl
16	3945	98.9	4683	US-10-696-282-1	Sequence 1, Appl
17	3945	98.9	4683	US-10-696-900-19	Sequence 19, Appl
18	3511	88.0	4722	US-10-427-129-3	Sequence 3, Appl
19	3494	87.6	4726	US-10-291-583-8	Sequence 8, Appl
20	3494	87.6	4726	US-10-959-017-4	Sequence 4, Appl
21	3473	87.1	3122	US-10-291-583-45	Sequence 45, Appl
22	3467	86.9	4382	US-10-496-799-1	Sequence 1, Appl
23	3464	86.8	3117	US-10-291-583-43	Sequence 43, Appl
24	3460	86.7	3121	US-10-291-583-44	Sequence 44, Appl
25	3457	86.7	3122	US-10-291-583-42	Sequence 42, Appl
26	3453	86.6	3128	US-10-291-583-27	Sequence 27, Appl
27	3451.5	86.5	3075	US-10-291-583-26	Sequence 26, Appl
28	3448	86.4	3129	US-10-291-583-25	Sequence 25, Appl
29	3446.5	86.4	3142	US-10-291-583-25	Sequence 25, Appl
30	3445	86.4	3123	US-10-291-583-41	Sequence 41, Appl
31	3442.5	86.3	4721	US-10-291-583-1	Sequence 1, Appl
32	3441	86.3	3128	US-10-291-583-47	Sequence 47, Appl
33	3440	86.2	3128	US-10-291-583-28	Sequence 28, Appl
34	3439	86.2	8179	US-10-205-942-5	Sequence 5, Appl
35	3438	86.2	3084	US-10-291-583-39	Sequence 39, Appl
36	3434	86.1	3086	US-10-291-583-37	Sequence 37, Appl
37	3432	86.0	3197	US-10-291-583-29	Sequence 29, Appl
38	3429	86.0	3121	US-10-291-583-11	Sequence 11, Appl
39	3424.5	85.8	3127	US-10-291-583-15	Sequence 15, Appl
40	3423.5	85.8	2205	US-10-291-583-120	Sequence 120, App
41	3423.5	85.8	4385	US-10-291-583-5	Sequence 5, Appl
42	3422.5	85.8	3095	US-10-291-583-24	Sequence 24, Appl
43	3422	85.8	3121	US-10-291-583-13	Sequence 13, Appl
44	3420.5	85.7	3113	US-10-291-583-31	Sequence 31, Appl
45	3420	85.7	3098	US-10-291-583-9	Sequence 9, Appl

## ALIGNMENTS

RESULT 1  
US-10-696-261-12  
; Sequence 12, Application US/10696261  
; Publication No. US20040057931A1  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James M.  
; APPLICANT: Xiao, Weidong  
; TITLE OF INVENTION: Adeno-Associated Virus Serotype 1 Nucleic Acid Sequences,  
; FILE REFERENCE: GNYPN.031USA  
; CURRENT APPLICATION NUMBER: US/10/696,261  
; PRIOR FILING DATE: 2003-10-29  
; PRIOR APPLICATION NUMBER: US/09/807,802A  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: US 60/107,114  
; PRIOR FILING DATE: 1998-11-05  
; PRIOR APPLICATION NUMBER: PCT/US99/25694  
; PRIOR FILING DATE: 1999-11-02  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 2211  
; TYPE: DNA  
; ORGANISM: AAV-1  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2208)  
; OTHER INFORMATION:  
US-10-696-261-12  
Alignment Scores:

GenCore version 5.1.6  
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OM protein - nucleic search, using: frameapp-us-p2n.model

Run on: December 12, 2005, 06:54:48 ; Search time 331 Seconds

(without alignments)  
3952.524 Million cell updates/sec

Title: US-10-696-282-13

Sequence: 1 MAADGVLPMEDLSEGR.....NGLYTRPRPIGTYLRPL 736

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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Database: Issued Patents NA.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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2	3989	100.0	4718	US-09-807-802A-11
3	3984	99.9	7447	US-10-216-870-11
4	3945	98.9	4683	US-09-807-802A-19
5	3439	86.2	8179	US-09-438-268-5
6	3402.5	85.3	4072	US-09-770-315-4
7	3402.5	85.3	4679	US-10-038-972A-12
8	3402.5	85.3	7557	US-09-770-315-3
9	3402.5	85.3	8698	US-09-770-315-2

10	3360.5	84.2	4680	2	US-08-254-358-1	Sequence 1, Appl1
11	3360.5	84.2	4680	2	US-08-475-391-1	Sequence 1, Appl1
12	3360.5	84.2	4680	2	US-08-709-609-1	Sequence 1, Appl1
13	3360.5	84.2	4680	6	PCT-US95-07178-1	Sequence 1, Appl1
14	3348.5	83.9	4681	3	US-09-807-802A-18	Sequence 1, Appl1
15	3322.5	83.3	4675	3	US-09-782-318A-1	Sequence 1, Appl1
16	3322.5	83.3	4675	3	US-09-782-318A-2	Sequence 1, Appl1
17	3251	81.5	1800	3	US-09-807-802A-14	Sequence 1, Appl1
18	3038.5	76.2	8151	3	US-09-438-268-2	Sequence 1, Appl1
19	2906	72.9	1605	3	US-09-807-802A-16	Sequence 1, Appl1
20	2494.5	62.5	7744	3	US-10-216-870-14	Sequence 1, Appl1
21	2486.5	62.3	2208	3	US-09-532-594B-5	Sequence 1, Appl1
22	2486.5	62.3	7214	3	US-09-438-268-1	Sequence 1, Appl1
23	2481.5	62.2	4767	3	US-09-533-427-1	Sequence 1, Appl1
24	2220	55.7	4652	3	US-09-533-427-7	Sequence 1, Appl1
25	2214	55.5	2264	3	US-09-533-427-8	Sequence 1, Appl1
26	2214	55.5	2264	3	US-09-533-427-8	Sequence 1, Appl1
27	2214	55.5	2264	3	US-09-533-427-8	Sequence 1, Appl1
28	1830.5	45.9	1800	3	US-09-532-594B-17	Sequence 1, Appl1
29	1690.5	42.4	1617	3	US-09-532-594B-19	Sequence 1, Appl1
30	1410	35.3	2271	3	US-09-438-268-3	Sequence 1, Appl1
31	599.5	15.0	2380	3	US-10-187-253E-26	Sequence 1, Appl1
32	599.5	15.0	2380	3	US-10-187-253E-32	Sequence 1, Appl1
33	599.5	15.0	4678	3	US-10-187-253E-22	Sequence 1, Appl1
34	599.5	15.0	4678	3	US-10-187-253E-22	Sequence 1, Appl1
35	486	12.2	1699	3	US-10-187-253E-28	Sequence 1, Appl1
36	486	12.2	1699	3	US-10-187-253E-28	Sequence 1, Appl1
37	439	11.0	5049	2	US-08-336-345-1	Sequence 1, Appl1
38	439	11.0	5049	2	US-08-336-345-2	Sequence 1, Appl1
39	439	11.0	5049	2	US-08-647-655-1	Sequence 1, Appl1
40	439	11.0	5049	2	US-08-647-655-2	Sequence 1, Appl1
41	277.5	7.0	681	3	US-10-187-253E-92	Sequence 1, Appl1
42	263	6.6	2062	9	5223424-3	Sequence 1, Appl1
43	247	6.2	1740	2	US-07-969-213-1	Sequence 1, Appl1
44	235.5	5.9	700	3	US-10-187-253E-4	Sequence 1, Appl1
45	233.5	5.9	700	3	US-10-187-253E-5	Sequence 1, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-807-802A-12  
Sequence 12, Application US/09807802A  
Patent No. 6759237  
GENERAL INFORMATION:  
APPLICANT: Watson, James M.  
TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,  
FILE REFERENCE: GNVFN.031USA  
CURRENT FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US/09/807,802A  
PRIOR FILING DATE: 1998-11-05  
PRIOR APPLICATION NUMBER: PCT/US99/25694  
PRIOR FILING DATE: 1999-11-02  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 12  
LENGTH: 2211  
TYPE: DNA  
ORGANISM: AAV-1  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(2208)  
OTHER INFORMATION:  
US-09-807-802A-12  
Alignment Scores:  
Pred. No.: 0  
Score: 3989.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Length: 2211  
Matches: 736  
Conservative: 0  
Mismatch: 0

GenCore version 5.1.6  
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OM protein - nucleic search, using ~~us-10-696-282-13~~ model

Run on: December 12, 2005, 06:00:53 : Search time 6192 Seconds  
(without alignments)  
5561.255 Million cell updates/sec

Title: US-10-696-282-13

Sequence score: 3989  
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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: gb\_est2:\*
- 3: gb\_est3:\*
- 4: gb\_hic:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_est7:\*
- 9: gb\_gse1:\*
- 10: gb\_gse2:\*
- 11: gb\_gse3:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 2	294	7.4	195	9	CO888893
C 3	193.5	4.9	753	9	BH115587
C 4	165	4.1	1944	10	AY415352
C 5	151.5	3.8	572	5	BM334595
C 6	148	3.7	1109	8	DR147327
C 7	147	3.7	2318	4	BC014681

8	139.5	3.5	803	9	B2265284
9	136.5	3.4	1297	4	CNS0FQWD
10	136	3.4	3945	4	CR749319
11	135	3.4	667	5	BM323619
12	134	3.4	856	5	BH164736
13	133	3.3	642	5	BM360495
14	133	3.3	1947	10	AY415350
15	133	3.3	2146	4	AK042727
16	133	3.3	3295	4	AK035953
17	130.5	3.3	2990	4	CR857451
18	130	3.3	687	4	BM482915
19	129	3.2	3943	4	AK087510
20	128.5	3.2	552	6	CF318715
21	128.5	3.2	4355	10	AY416870
22	128	3.2	921	10	CG239378
23	127.5	3.2	1902	4	CR602498
24	127.5	3.2	2613	11	DQ052183
25	127.5	3.2	5021	4	CR857584
26	125	3.1	640	6	CA356072
27	125	3.1	701	6	CA378088
28	125	3.1	703	6	CA378088
29	125	3.1	745	2	BJ139005
30	125	3.1	754	2	BC207226
31	125	3.1	2019	4	AK014322
32	124	3.1	925	5	BQ440075
33	123.5	3.1	925	5	BI911451
34	123.5	3.1	645	4	CR591190
35	123.5	3.1	3512	4	AK038988
36	123.5	3.1	4763	4	AK083225
37	123	3.1	631	5	BM328301
38	123	3.1	6987	4	BC069829
39	122.5	3.1	703	7	CF869635
40	122.5	3.1	756	9	AQ742711
41	122.5	3.1	795	6	CB899782
42	122.5	3.1	2391	10	CL961669
43	122.5	3.1	2610	11	DQ052184
44	122	3.1	4180	4	HSN801295
45	121.5	3.0	925	9	BH152154

#### ALIGNMENTS

RESULT 1  
LOCUS CO892248/c 264 bp mRNA linear EST 01-SEP-2004  
DEFINITION BOVEN.20573 normal cattle brain Bos taurus cDNA clone  
R2PDP1056W0360Q 5', mRNA sequence.

ACCESSION CO892248  
VERSION CO892248.1 GI:51822548

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus  
Bos taurus  
Bukariyoca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 264)  
Hennig, S., Janitz, M., Herwig, R. and Williams, J.  
Generation, annotation, evolutionary analysis and database  
integration of 14969 cattle EST clusters  
Unpublished (2004)

JOURNAL COMMENT  
Contact: Hennig S  
laboratory 123, dept. Lehrach  
Max-Planck-Institut fuer Molekulare Genetik  
Innestr. 63-73, D-14195 Berlin, Germany  
Tel: +49 30 8413 1612  
Fax: +49 30 8413 1380

Email: hennig@molgen.mpg.de  
The library was characterized by oligonucleotide fingerprinting  
(ONFP) to reduce sequencing redundancy. According to the ONFP  
procedure, clones that display the same hybridization matrix with a  
battery of 200 8mer oligonucleotides are grouped into clusters. One  
clone per ONFP cluster was selected for sequencing. cDNA clones and  
filters are distributed via Deutsches Reesourcenzentrum fuer

GenCore version 5.1.6  
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# OM protein - nucleic search,

Using frameplus p2n model

Run on: December 12, 2005, 00:05:58 ; Search time 974 Seconds

(without alignments)  
5036.154 Million cell updates/sec

Title: US-10-696-282-13

Sequence: 1 MADDGTLPMLENDLSEGR.....NGLYEPRIPIGRYLRPL 736

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Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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13: geneseg2004bs:\*  
14: geneseg2005s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	3989	100.0	2211	14 AD227052	Ad227052 Adeno-ss
3	3989	100.0	2211	14 AD226899	Ad226899 Adeno-ss
4	3989	100.0	4347	13 ADM39398	Adm39398 Adeno-ss

5	3989	100.0	4347	14 AD246594	Ad246594 HSV-AAV s
6	3989	100.0	4718	3 AAD00772	Aad00772 Adeno-ss
7	3989	100.0	4718	10 AD276507	Ad276507 Adeno-ss
8	3989	100.0	4718	10 ADL13984	Adl13984 Adeno-ss
9	3989	100.0	4718	12 ADG39758	Adg39758 AAV-1 gen
10	3984	99.9	7447	8 ACC58477	Acc58477 Vector pf
11	3968	99.5	2211	14 AD226928	Ad226928 Adeno-ss
12	3963	99.3	2211	14 AD227053	Ad227053 Adeno-ss
13	3963	99.3	4239	13 ADM39402	Adm39402 Adeno-ss
14	3963	99.3	4239	14 AD246598	Ad246598 HSV-AAV s
15	3963	99.3	4683	4 AAP23749	Aaf23749 AAV6 DNA
16	3963	99.3	4683	10 ADL13983	Adl13983 Adeno-ss
17	3963	99.3	4683	12 ADG39763	Adg39763 AAV-6 gen
18	3883.5	97.4	2214	14 AD226931	Ad226931 Adeno-ss
19	3873	97.1	2211	14 AD226931	Ad226931 Adeno-ss
20	3853	96.6	2211	14 AD226932	Ad226932 Adeno-ss
21	3511	88.0	4722	4 AAP23748	Aaf23748 AAV3B DNA
22	3511	88.0	4722	12 ADG39760	Adg39760 AAV-3B ge
23	3494	87.6	2211	14 AD227050	Ad227050 Adeno-ss
24	3494	87.6	4286	14 AD246595	Ad246595 HSV-AAV s
25	3494	87.6	4287	13 ADM39399	Adm39399 Adeno-ss
26	3494	87.6	4726	10 AD276509	Ad276509 Adeno-ss
27	3494	87.6	4726	10 ADL13985	Adl13985 Adeno-ss
28	3494	87.6	4726	12 ADG39759	Adg39759 AAV-3A ge
29	3483.5	87.3	2214	14 AD226891	Ad226891 Adeno-ss
30	3473	87.1	3122	10 AD276546	Ad276546 Adeno-ss
31	3469	87.0	2217	14 AD226892	Ad226892 Adeno-ss
32	3467	86.9	4382	9 ABG80410	Abg80410 AAV9 rep
33	3464	86.8	3117	10 AD276544	Ad276544 Adeno-ss
34	3460	86.7	3121	10 AD276545	Ad276545 Adeno-ss
35	3458.5	86.7	2214	14 AD226886	Ad226886 Adeno-ss
36	3457	86.7	3122	10 AD276543	Ad276543 Adeno-ss
37	3456.5	86.7	2214	14 AD226885	Ad226885 Adeno-ss
38	3456.5	86.7	2214	14 AD226885	Ad226885 Adeno-ss
39	3456.5	86.7	2217	14 AD227020	Ad227020 Adeno-ss
40	3456	86.6	3158	14 AD226889	Ad226889 Adeno-ss
41	3455.5	86.6	2214	14 AD226882	Ad226882 Adeno-ss
42	3453.5	86.6	2208	14 AD226895	Ad226895 Adeno-ss
43	3453.5	86.6	2208	14 AD226895	Ad226895 Adeno-ss
44	3453	86.6	2217	14 AD226863	Ad226863 Adeno-ss
45	3453	86.6	2217	14 AD226859	Ad226859 Adeno-ss

## ALIGNMENTS

RESULT 1	
AAD00777	
ID AAD00777 standard; DNA; 2211 BP.	
XX	
AC AAD00777;	
XX	
DT 08-SEP-2000 (first entry)	
XX	
DE Adeno-associated virus serotype 1 capsid protein VP1 DNA.	
XX	
KM Adeno-associated virus serotype 1; AAV-1; rep protein; capsid protein;	
KW cap protein; recombinant viral vector; gene delivery; gene therapy;	
XX vaccine; transgene; VP1; ss.	
OS Adeno associated virus serotype 1.	
XX	
PH Key	Location/Qualifiers
FT CDS	1..2211
FT	/tag= a
FT	/product= "VP1 protein"
XX	
PN WO200028061-A2.	
XX	
PD 18-MAY-2000.	
XX	
PF 02-NOV-1999; 99WO-US025694.	
XX	
PR 05-NOV-1998; 98US-0107114P.	



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OM protein - nucleic search, using frame3p2nmodel.rge

Run on: December 12, 2005, 05:57:53 ; Search time 8511 Seconds

(without alignments)  
4915.613 Million cell updates/sec

Title: US-10-696-282-13

Sequence: 1 MANDGYLPDMEDLSEGR.....NGLYTERPRIGTYLRPL 736

Scoring table:

BIOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delpop 6.0 , Delpext 7.0	

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODEL=frame3.p2n.model -DEV=xlp  
-O=/cgn2.1/USPTO.spool.P/US10656282/runat.06122005.133342.8409/app.query.fasta\_1.90  
-DB=GenBank -OFT=fasta -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pro -NOR=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10656282.CCN.1.1.7415 @runat.06122005.133342.8409 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDP=6 -DELEXT=7

Database :

GenBank:.\*  
1: gb\_ba:.\*  
2: gb\_in:.\*  
3: gb\_env:.\*  
4: gb\_cm:.\*  
5: gb\_ov:.\*  
6: gb\_pat:.\*  
7: gb\_ph:.\*  
8: gb\_pr:.\*  
9: gb\_rc:.\*  
10: gb\_stc:.\*  
11: gb\_sy:.\*  
12: gb\_un:.\*  
13: gb\_vl:.\*  
14: gb\_hlg:.\*  
15: gb\_pl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARYS

Result No.	Score	Query Match	Length	DB ID	Description
1	3989	100.0	2211	6	BD242771 Adeno-ss
2	3989	100.0	2211	6	CS073491 Sequence
3	3989	100.0	2211	6	CS073614 Sequence

Result No.	Score	Query Match	Length	DB ID	Description
4	3989	100.0	2211	6	ARS62503 Sequence
5	3989	100.0	4718	6	BD242766 Adeno-ss
6	3989	100.0	4718	6	ARS62498 Sequence
7	3989	100.0	4718	6	AX753251 Sequence
8	3989	100.0	4718	13	AF063497 Adeno-ss
9	3984	99.9	7447	6	ARS27492 Sequence
10	3968	99.5	2211	6	CS073490 Sequence
11	3968	99.5	2211	13	AY530611 Adeno-ss
12	3963	99.3	2211	6	CS073615 Sequence
13	3963	99.3	4683	13	AF028704 Adeno-ss
14	3945	98.9	4683	6	BD242775 Adeno-ss
15	3945	98.9	4683	6	ARS62507 Sequence
16	3883.5	97.4	2214	6	CS073492 Sequence
17	3883.5	97.4	2214	13	AY530606 Adeno-ss
18	3873	97.1	2211	6	CS073493 Sequence
19	3873	97.1	2211	13	AY530607 Adeno-ss
20	3853	96.6	2211	6	CS073494 Sequence
21	3853	96.6	2211	13	AY530609 Adeno-ss
22	3511	88.0	4722	13	AF028705 Adeno-ss
23	3494	87.6	2211	6	CS073612 Sequence
24	3494	87.6	4726	6	AX753253 Sequence
25	3494	87.6	4726	13	AY048704 Adeno-ss
26	3483.5	87.3	2214	6	CS073453 Sequence
27	3473	87.1	2211	13	AY242997 Non-human
28	3473	87.1	3122	6	AX753290 Sequence
29	3469.5	87.0	4430	13	AY695376 Adeno-ss
30	3469	87.0	2217	6	CS073454 Sequence
31	3464	86.8	3117	6	AX753288 Sequence
32	3460	86.7	3121	6	AX753289 Sequence
33	3458.5	86.7	2214	6	CS073448 Sequence
34	3457	86.7	3122	6	AX753287 Sequence
35	3456.5	86.7	2208	13	AY530622 Adeno-ss
36	3456.5	86.7	2214	6	CS073447 Sequence
37	3456.5	86.7	2214	6	CS073452 Sequence
38	3456.5	86.7	2214	13	AY530567 Adeno-ss
39	3456.5	86.7	3158	6	CS073582 Sequence
40	3456	86.6	2217	6	CS073431 Sequence
41	3455.5	86.6	2214	6	CS073444 Sequence
42	3455.5	86.6	2214	13	AY530561 Adeno-ss
43	3453.5	86.6	2208	6	CS073457 Sequence
44	3453.5	86.6	2208	6	CS073461 Sequence
45	3453.5	86.6	2208	13	AY530591 Adeno-ss

## ALIGNMENTS

RESULT 1  
BD242771 2211 bp DNA linear PAT 17-JUL-2003  
LOCUS Adeno-associated virus serum type 1 nucleic acid sequence, vector  
DEFINITION Adeno-associated virus serum type 1 nucleic acid sequence, vector  
ACCESSION BD242771  
VERSION BD242771.1 GI:33052541  
KEYWORDS JP 2002529098-A/6.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 2211)  
AUTHORS Wilson,T.M. and Xiao,W.  
TITLE Adeno-associated virus serum type 1 nucleic acid sequence, vector  
JOURNAL and host cell containing the same  
PATENT: JP 2002529098-A 6 10-SEP-2002;  
COMMENT THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA  
OS AYV-1  
PN JP 2002529098-A/6  
PD 10-SEP-2002 JP 2000581227  
PR 02-NOV-1999 JP 2000581227  
PR 05-NOV-1998 US 60/107114  
PI JAMES M WILSON, WEIDONG XIAO  
PC C12N15/09,A61K31/711,A61K48/00,A61P43/00,C12N1/15,C12N1/19, PC  
C12N1/21,  
PC C12N5/10,C12P21/02//A61K35/76,C12N15/00,C12N5/00 CC  
Adeno-associated virus serum type 1 nucleic acid sequence, CC





QY	1	TTGCGCACTCCCTCTGCGCGCTGCTGCTGCTGCGGACCTTGCGGACCAAAAGTCCGC	60
Db	1	TTGCCCACTCCCTCTGCGCGCTGCTGCTGCTGCGGACCTTGCGGACCAAAAGTCCGC	60
QY	61	AGACGCGCAGAGCTGCTCTGCGCGGCCCAACGACGACAGCGCCGACAGAGGGAGTG	120
Db	61	AGACGCGCAGAGCTCTGCTCTGCGCGGCCCAACGACGACAGCGCCGACAGAGGGAGTG	120
QY	121	GGCAACTCCATCACTAGGGGTAAATGGCGAAGGCGCTCCCAAGTCCGCGCGCAGCGCTGA	180
Db	121	GGCAACTCCATCACTAGGGGTAAATGGCGAAGGCGCTCCCAAGTCCGCGCGCAGCGCTGA	180
QY	181	CGTAAATTACGTCAATAGGGGAGTGGTCTGTATTAGCTGTACAGCTGAGTCCCTTTGGCAC	240



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OM nucleic - nucleic search, using sw model

Run on: December 11, 2005, 12:04:41, Search time 16217 Seconds  
(without alignment)  
13611.732 Million cell updates/sec

Title: US-10-696-282-1

Perfect score: 4718  
Sequence: 1 ctgccactccctctcgcg.....cgagagagggagtcggca 4718

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 239354128 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_est3:  
4: gb\_hic:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_est7:  
9: gb\_gsa1:  
10: gb\_gsa2:  
11: gb\_gsa3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	180.8	3.8	264	7	CO892248
C 2	126.8	2.7	195	7	CO888893
C 3	91.8	1.9	489	9	AZ289042
C 4	85.4	1.8	778	10	AG491391
C 5	76.2	1.6	753	9	BH115587
C 6	71	1.5	495	9	AZ028362
C 7	60.6	1.3	668	7	CF843972
C 8	55.6	1.2	636	3	BM440166
C 9	55.2	1.2	659	3	BM371945
C 10	55.2	1.2	692	5	BQ766288
C 11	55.2	1.2	852	2	BG310300
C 12	55.2	1.2	869	3	BP170704
C 13	55.2	1.2	1553	8	DN551925
C 14	54.6	1.2	845	7	CK462848
C 15	54.4	1.2	665	5	BM846578
C 16	54.4	1.1	415	5	CA024206
C 17	54	1.1	638	3	BQ550744
C 18	54	1.1	652	3	BQ268130
C 19	54	1.1	734	5	BU093182
C 20	54	1.1	818	9	BZ578035
C 21	54	1.1	1125	8	DR736937
C 22	53.8	1.1	878	6	CD437318

23	53.2	1.1	556	10	CM491633
24	53.2	1.1	607	5	BQ60503
25	53.2	1.1	700	10	CM041764
26	53	1.1	714	7	CF846078
27	52.6	1.1	484	9	CE239279
28	52.6	1.1	694	7	CF843324
29	52.6	1.1	818	6	CB800543
30	52.6	1.1	818	7	CF870364
31	52.4	1.1	528	1	AL818251
32	52.4	1.1	688	3	BM816637
33	52.4	1.1	837	8	CV776978
34	52.4	1.1	1065	4	AV110092
35	52.4	1.1	1092	8	DR741775
36	52.2	1.1	942	7	CK371427
37	52.2	1.1	938	10	CG329376
38	52	1.1	729	10	CL971124
39	52	1.1	859	6	CA174679
40	52	1.1	877	3	BI952167
41	51.8	1.1	645	6	CB479173
42	51.6	1.1	492	6	CF487798
43	51.6	1.1	570	2	BA452865
44	51.6	1.1	577	6	CF487880
45	51.6	1.1	612	3	BI873856

#### ALIGNMENTS

RESULT 1  
LOCUS CO892248/C 264 bp mRNA linear EST 01-SEP-2004  
DEFINITION Bovgen\_20573 normal cattle brain Bos taurus cDNA clone  
RZPDp1056M0360Q 5', mRNA sequence.  
ACCESSION CO892248  
VERSION CO892248.1 GI:51822548  
KEYWORDS EST  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Bovora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 264)  
Hennig,S., Janitz,M., Herwig,R. and Williams,J.  
Generation, annotation, evolutionary analysis and database  
integration of 14969 cattle EST clusters  
Unpublished (2004)  
Contact: Hennig S  
laboratory 123, dept.Lehrach  
Max-Planck-Institut fuer Molekulare Genetik  
Inhestr.63-73, D-14195 Berlin, Germany  
Tel: +49 30 8413 1612  
Fax: +49 30 8413 1380  
Email: hennig@molgen.mpg.de  
The library was characterised by oligonucleotide fingerprinting  
(ONPF) to reduce sequencing redundancy. According to the ONPF  
procedure, clones that display the same hybridisation matrix with a  
battery of 200 8mer oligonucleotides are grouped into clusters. One  
clone per ONPF cluster was selected for sequencing. cDNA clones and  
filters are distributed via Deutsches Ressourcenzentrum fuer  
Genomforschung GmbH (http://www.rzpd.de).

PCR Primers  
FORWARD: 5' -CCCCAGGCTTACCTTATGCTCCGGCTCG 3' (M13RSP) 5'-seq  
BACKWARD: 5' -GCTATTACGACGACGACGGAAGGCGATGTG 3' (M13SP) 3'-seq  
Seq primer: 5' -CCGGTCGGAATTCGCCGGT-3' (M13RSP).

#### FEATURES

Location/Qualifiers  
1..264  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/clone="RZPDp1056M0360Q"  
/sex="female"  
/tissue\_type="brain tissue"  
/dev\_stage="adult brain"

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OM nucleic - nucleic search, using bw model

Run on: December 11, 2005, 10:59:26 ; Search time 2451 Seconds

(without alignments)  
12829.057 Million cell updates/sec

Title: US-10-696-282-1

Perfect score: 4718

Sequence: 1 ttcgccaccctccctctcg...

Scoring table: IDENTITY NUC

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4718	100.0	4718	3	Adeno-888
2	4718	100.0	4718	10	Adeno-888
3	4718	100.0	4718	10	Adeno-888
4	4718	100.0	4718	12	Adeno-888
5	4258	90.3	4683	4	Adeno-888
6	4258	90.3	4683	10	Adeno-888
7	3947.4	83.7	4721	10	Adeno-888
8	3947.4	83.7	4721	12	Adeno-888
9	3947.4	83.7	4721	14	Adeno-888
10	3947.4	83.7	4721	14	Adeno-888
11	3947.4	83.7	4721	14	Adeno-888
12	3947.4	83.7	4721	14	Adeno-888
13	3947.4	83.7	4721	14	Adeno-888
14	3947.4	83.7	4721	14	Adeno-888
15	3947.4	83.7	4721	14	Adeno-888
16	3947.4	83.7	4721	14	Adeno-888
17	3947.4	83.7	4721	14	Adeno-888
18	3947.4	83.7	4721	14	Adeno-888
19	3947.4	83.7	4721	14	Adeno-888

20	3546.4	75.2	4393	12	Adeno-888
21	3546.4	75.2	4393	14	Adeno-888
22	3546.4	75.2	4393	14	Adeno-888
23	3546.4	75.2	4393	14	Adeno-888
24	3211.6	68.1	4726	10	Adeno-888
25	3211.6	68.1	4726	10	Adeno-888
26	3205	67.9	4722	12	Adeno-888
27	3205	67.9	4722	12	Adeno-888
28	3107.8	65.9	4679	6	Adeno-888
29	3107.8	65.9	4679	6	Adeno-888
30	3107.8	65.9	4679	10	Adeno-888
31	3107.8	65.9	4679	14	Adeno-888
32	3107.8	65.9	4679	14	Adeno-888
33	3106.2	65.8	4679	4	Adeno-888
34	3096.6	65.6	4679	12	Adeno-888
35	3082.4	65.3	4680	2	Adeno-888
36	3082.4	65.3	4680	8	Adeno-888
37	3082.4	65.3	4680	9	Adeno-888
38	3082.4	65.3	4680	10	Adeno-888
39	3082.4	65.3	4680	12	Adeno-888
40	3082.4	65.3	4680	14	Adeno-888
41	3055.8	64.8	4675	4	Adeno-888
42	3055.8	64.8	4675	4	Adeno-888
43	3055.8	64.8	4675	6	Adeno-888
44	3055.8	64.8	4675	6	Adeno-888
45	3055.8	64.8	4675	6	Adeno-888

#### ALIGNMENTS

RESULT 1	AAD00772	standard; DNA; 4718 BP.
ID	AAD00772	
AC	AAD00772	
DT	08-SEP-2000	(first entry)
XX	Adeno-associated virus serotype 1 DNA.	
DE	Adeno-associated virus serotype 1 DNA.	
XX	Adeno-associated virus serotype 1; AAV-1; rep protein; capsid protein; cap protein; recombinant viral vector; gene delivery; gene therapy; vaccine; transgene; ss.	
OS	Adeno associated virus serotype 1.	
XX	Key	Location/Qualifiers
FT	repeat_unit	1..143
FT		/tag= a
FT		/note= "Inverted terminal repeat which is capable of forming T-shaped hairpin structure"
FT	protein_bind	89..110
FT		/tag= b
FT	misc_feature	124..125
FT		/note= "Rep protein"
FT	misc_binding	219..226
FT		/tag= c
FT		/note= "Terminal residue site (TRS)"
FT		/tag= d
FT		/bound_moiety= "USF"
FT	promoter	236..299
FT		/tag= e
FT		/label= p5_promoter
FT	protein_bind	237..245
FT		/tag= f
FT		/bound_moiety= "YY1 factor"
FT	TATA_signal	270..275
FT		/tag= g
FT		/label= p5_TATA-Box
FT	misc_feature	299..306

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OM nucleic - nucleic search, using sw model

Run on: December 11, 2005, 12:02:06 ; Search time 22657 Seconds  
(without alignments)  
11836.845 Million cell updates/sec

Title: US-10-696-282-1

Perfect score: 4718  
Sequence: 1 ttcgccacacccctctctgcg.....cgcagagaggaagtgggcaa 4718

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenBml:\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_cm:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_str:\*  
11: gb\_sv:\*  
12: gb\_un:\*  
13: gb\_vl:\*  
14: gb\_hcg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4718	100.0	4718	6	BD242766 Adeno-ss
2	4718	100.0	4718	6	AR562498 Sequence
3	4718	100.0	4718	6	AX753251
4	4718	100.0	4718	13	AP063497
5	4258	90.3	4683	13	AP028704
6	4253.2	90.1	4683	6	BD242775 Adeno-ss
7	4253.2	90.1	4683	6	AR562507 Sequence
8	3947.4	83.7	4721	6	CQ972062 Sequence
9	3947.4	83.7	4721	6	CS073592 Sequence
10	3947.4	83.7	4721	6	AX753246 Sequence
11	3947.4	83.7	4721	13	AF513851
12	3587.2	76.0	4385	6	AX753250
13	3546.4	75.2	4393	6	CQ972063 Sequence
14	3546.4	75.2	4393	6	CS073594 Sequence
15	3546.4	75.2	4393	6	AX753249 Sequence
16	3546.4	69.8	4393	13	AF513852
17	3293.8	69.8	4102	13	AY631965
18	3211.6	68.1	4726	6	AX753253

19	3211.6	68.1	4726	13	AV048704	U48704 Adeno-ss
20	3205	67.9	4722	13	AF028705	AF028705 Adeno-ss
21	3107.8	65.9	4679	6	AX282480	AX282480 Sequence
22	3107.8	65.9	4679	13	AF043303	AF043303 Adeno-ss
23	3107.8	65.9	8698	6	AR222044	AR222044 Sequence
24	3107.8	65.9	8698	6	AX205072	AX205072 Sequence
25	3084.2	65.4	4681	6	BD242774	BD242774 Adeno-ss
26	3084.2	65.4	4681	6	AR562506	AR562506 Sequence
27	3082.4	65.3	4680	6	AR028767	AR028767 Sequence
28	3082.4	65.3	4680	6	162303	162303 Sequence 1
29	3055.8	64.8	4675	6	BD094552	BD094552 Method of
30	3055.8	64.8	4675	6	AX135805	AX135805 Sequence
31	3055.8	64.8	4675	6	AX286292	AX286292 Sequence
32	3055.8	64.8	4675	6	AX753252	AX753252 Sequence
33	3055.8	64.8	4675	13	AA2CG	J01801 Adeno-ss
34	2993.4	63.4	7557	6	AR222045	AR222045 Sequence
35	2993.4	63.4	7557	6	AX205073	AX205073 Sequence
36	2972.6	63.0	4429	13	AY695371	AY695371 Adeno-ss
37	2971	63.0	4429	13	AY695372	AY695372 Adeno-ss
38	2969.6	62.9	4430	13	AY695376	AY695376 Adeno-ss
39	2963.2	62.8	4430	13	AY695374	AY695374 Adeno-ss
40	2961.4	62.8	4429	13	AY695373	AY695373 Adeno-ss
41	2959.8	62.7	4429	13	AY695375	AY695375 Adeno-ss
42	2941.8	62.4	8179	6	BD271148	BD271148 Virus vec
43	2941.8	62.4	8179	6	AR264580	AR264580 Sequence
44	2878.4	61.0	7337	11	AF369663	AF369663 Cloning v
45	2731	57.9	4087	13	AY631966	AY631966 Adeno-ss

## ALIGNMENTS

RESULT 1	BD242766	4718 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD242766				
DEFINITION	Adeno-associated virus serum type 1 nucleic acid sequence, vector				
ACCESSION	BD242766				
VERSION	BD242766.1	GI:33052536			
KEYWORDS	JP 2002529098-A/1.				
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 4718)				
AUTHORS	Wilson, J.M. and Xiao, W.				
TITLE	Adeno-associated virus serum type 1 nucleic acid sequence, vector				
JOURNAL	and host cell containing the same				
COMMENT	Patent: JP 2002529098-A 1 10-SEP-2002;				
	THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA				
	OS AAV-1				
	PN JP 2002529098-A/1				
	PD 10-SEP-2002				
	PF 02-NOV-1999 JP 200581227				
	PR 05-NOV-1998 US 60/107114				
	PI JAMES M WILSON, WEIDONG XIAO				
	PC C12N15/09,A61K31/711,A61K48/00,A61P43/00,C12N1/15,C12N1/19, PC				
	C12N1/21.				
	PC C12N5/10,C12P21/02//A61K35/76,C12N15/00,C12N5/00 CC				
	Adeno-associated virus serum type 1 nucleic acid sequence, CC				
	vector and host				
	CC cell containing the same				
	FT Key location/Qualifiers				
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	FT CDS (2223)..(4430).				
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	/db_xref="taxon:32644"				
ORIGIN					
Query Match	100.0%; Score 4718; DB 6; Length 4718;				
Best Local Similarity	100.0%; Pred. No. 0;				